

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model
Run on: February 1, 2006, 10:41:26 ; Search time 142 Seconds

US-10-604-944A-14
Perfect score: 77
Sequence: ttacccatatacgacaa.....aactttaatgcgtggtaa 77
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2605114
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2_6/prodata/1/ina/1_COMB.seq: *
2: /cgn2_6/prodata/1/ina/5_COMB.seq: *
3: /cgn2_6/prodata/1/ina/6A_COMB.seq: *
4: /cgn2_6/prodata/1/ina/B_COMB.seq: *
5: /cgn2_6/prodata/1/ina/H_COMB.seq: *
6: /cgn2_6/prodata/1/ina/P_COMB.seq: *
7: /cgn2_6/prodata/1/ina/R_COMB.seq: *
8: /cgn2_6/prodata/1/ina/backfilesl.seq: *
9: /cgn2_6/prodata/1/ina/backfilesl.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	77	100.0	840	2 US-07-979-966A-1
2	77	100.0	845	2 US-08-589-463-3
3	77	100.0	845	2 US-08-444-882-3
4	77	100.0	845	2 US-08-389-559A-3
5	77	100.0	845	3 US-08-987-667A-3
6	77	100.0	1314	3 US-08-392-794A-1
7	77	100.0	2095	2 US-08-333-901-5
8	77	100.0	2095	2 US-08-456-882-5
9	77	100.0	2095	2 US-08-898-789-5
10	77	100.0	3807	2 US-08-417-710A-7B
11	77	100.0	3807	3 US-08-463-209-5
12	77	100.0	4307	3 US-09-552-950-1
13	77	100.0	4307	3 US-09-936-572-1
14	77	100.0	4338	3 US-09-872-733A-1
15	77	100.0	5362	3 US-08-463-210-5
16	77	100.0	5362	3 US-08-463-028-5
17	77	100.0	5362	3 US-08-463-209-5
18	77	100.0	7228	2 US-08-850-049-128
19	77	100.0	7228	2 US-08-850-149-128
20	77	100.0	7228	2 US-08-850-178-128
21	77	100.0	7228	2 US-08-050-478-129
22	77	100.0	7228	3 US-09-414-117-128
23	77	100.0	7228	3 US-09-414-117-128
24	77	100.0	7228	3 US-09-678-437-129
25	77	100.0	7228	3 US-09-678-437-129
26	77	100.0	7228	3 US-09-943-722-128
27	77	100.0	7228	3 US-09-943-722-128
28	77	100.0	8366	3 US-09-872-733A-6
29	77	100.0	8560	3 US-09-936-572-11
30	77	100.0	8932	3 US-09-124-900-1
31	77	100.0	8933	3 US-08-463-210-4
32	77	100.0	8933	3 US-09-620-958A-3
33	77	100.0	8933	3 US-09-620-958A-4
34	77	100.0	8933	3 US-09-620-958A-9
35	77	100.0	8933	3 US-08-463-028-4
36	77	100.0	8933	3 US-08-463-209-4
37	77	100.0	8933	3 US-09-943-286-3
38	77	100.0	8933	3 US-09-943-286-4
39	77	100.0	8933	3 US-09-943-286-9
40	77	100.0	9609	3 US-09-827-688-4
41	77	100.0	9719	3 US-09-700-304-1
42	75.4	97.9	1503	3 US-09-393-795-2
43	75.4	97.9	7399	2 US-08-418-848A-9
44	75.4	97.9	9709	2 US-08-188-583-5
45	75.4	97.9	9709	3 US-08-388-353-1

ALIGNMENTS

Sequence 129, APP
Sequence 128, APP
Sequence 129, APP
Sequence 6, Appli
Sequence 11, Appli
Sequence 1, Appli
Sequence 4, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 9, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 9, Appli
Sequence 4, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 9, Appli
Sequence 5, Appli
Sequence 1, Appli

RESULT 1
US-07-979-966A-1
; Sequence 1, Application US/07979966A
; Patent No. 5707864
GENERAL INFORMATION:
; APPLICANT: Myron E. Essex
; APPLICANT: Xiaofang Yu
; APPLICANT: Yun-Hou Lee
TITLE OF INVENTION: AIDS THERAPEUTICS BASED ON HIV
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/979_966A
FILING DATE: NO. 5707864ember 23, 1992
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: John W. Freeman
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00379/018001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 840
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-07-979-966A-1

Query Match 100.0%; Score 77; DB 2; Length 840;

EDT

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Om nucleic - nucleic search, using SW model

Run on: February 1, 2006, 10:44:30 ; Search time 816 Seconds
 (without alignments)
 780.321 Million cell updates/sec

Title: US-10-604-944A-14
 Perfect score:
 Sequence: 1 ttacctatagtcagaaca.....aaccttaatgcatggtaa 77

Scoring table: IDENTITY_NTC
 Gapop 10⁻⁰, Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications NA Main:*

1: /cggn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq: *
 2: /cggn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq: *
 3: /cggn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq: *
 4: /cggn2_6/ptodata/1/pubpna/US1A_PUBCOMB.seq: *
 5: /cggn2_6/ptodata/1/pubpna/US1B_PUBCOMB.seq: *
 6: /cggn2_6/ptodata/1/pubpna/US1C_PUBCOMB.seq: *
 7: /cggn2_6/ptodata/1/pubpna/US1D_PUBCOMB.seq: *
 8: /cggn2_6/ptodata/1/pubpna/US1E_PUBCOMB.seq: *
 9: /cggn2_6/ptodata/1/pubpna/US1L_PUBCOMB.seq: *
 10: /cggn2_6/ptodata/1/pubpna/US1L_PUBCOMB.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	77	100.0	77	8 US-10-604-944-14 Sequence 14, Appl
2	77	100.0	845	3 US-09-756-51A-3 Sequence 3, Appl
3	77	100.0	1092	5 US-10-003-035-34 Sequence 34, Appl
4	77	100.0	1092	6 US-10-286-332A-34 Sequence 34, Appl
5	77	100.0	1092	6 US-10-280-915-34 Sequence 34, Appl
6	77	100.0	1092	8 US-10-286-332A-34 Sequence 34, Appl
7	77	100.0	1092	8 US-10-080-915-34 Sequence 34, Appl
8	77	100.0	1179	5 US-10-003-035-35 Sequence 35, Appl
9	77	100.0	1179	6 US-10-286-332A-35 Sequence 35, Appl
10	77	100.0	1179	6 US-10-080-915-35 Sequence 35, Appl
11	77	100.0	1179	8 US-10-286-332A-35 Sequence 35, Appl
12	77	100.0	1179	8 US-10-280-915-35 Sequence 35, Appl
13	77	100.0	1308	5 US-10-003-035-36 Sequence 36, Appl
14	77	100.0	1308	6 US-10-286-332A-36 Sequence 36, Appl
15	77	100.0	1308	6 US-10-286-915-36 Sequence 36, Appl
16	77	100.0	1308	8 US-10-286-332A-36 Sequence 36, Appl
17	77	100.0	1308	8 US-10-280-915-36 Sequence 36, Appl
18	77	100.0	1308	5 US-10-003-035-17 Sequence 17, Appl
19	77	100.0	1496	6 US-10-286-332A-17 Sequence 17, Appl
20	77	100.0	1496	6 US-10-280-915-17 Sequence 17, Appl
21	77	100.0	1496	8 US-10-286-332A-17 Sequence 17, Appl
22	77	100.0	1496	8 US-10-280-915-17 Sequence 17, Appl
23	100.0	1503	3 US-09-968-355-22 Sequence 22, Appl	

ALIGNMENTS

RESULT 1
 US-10-604-944-14
 ; Sequence 14, Application US/10604944
 ; Publication No. US20040219515A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ROSETTA GENOMICS LTD
 ; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL HIV REGULATORY GENE;
 ; TITLE OF INVENTION: AND USES THEREOF
 ; FILE REFERENCE: 55008
 ; CURRENT APPLICATION NUMBER: US/10/604,944
 ; CURRENT FILING DATE: 2003-08-28
 ; NUMBER OF SEQ ID NOS: 406
 ; SOFTWARE: Patentin version 3.2
 ; SEQ ID NO 14
 ; LENGTH: 77
 ; TYPE: DNA
 ; ORGANISM: Human immunodeficiency virus 1
 US-10-604-944-14

Query Match 100.0%; Score 77; DB 8; length 77;
 Best Local Similarity 100.0%; Pred. No. 2.7e-18;
 Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTACCTATAGTCAGACATCCAGGGCAATGCTACAGGCCATATCACCTAGAAC 60
 Db 1 TTACCTATAGTCAGACATCCAGGGCAATGCTACAGGCCATATCACCTAGAAC 60

Qy 61 TTAAATGCAATGGTA 77
 Db 61 TTAAATGCAATGGTA 77

RESULT 2
 US-09-756-51A-3
 ; Sequence 3, Application US/09756551A
 ; Patent No. US2002005168A1
 ; GENERAL INFORMATION:
 ; APPLICANT: C. MORROW et al.
 ; TITLE OF INVENTION: ENCAPSULATED RECOMBINANT VIRAL
 ; TITLE OF INVENTION: NUCLEIC ACID AND METHODS OF MAKING AND
 ; TITLE OF INVENTION: USING SAME
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSE: LARKE & COCKFIELD
 ; STREET: 28 STATE STREET
 ; CITY: BOSTON

(6) J

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OM nucleic - nucleic search, using sw model

Run on: February 1, 2006, 10:38:36 ; Search time 483 Seconds
(without alignments)

Title: US-10-604-944A-14

Perfect score: 77

Sequence: 1 ttacccatagtgcgaaaca.....aactttaatgcatggtaa 77

Scoring table: IDENTITY_NUC
Gapext 10⁻⁰, Gapext 1.0

Searched: 4996997 seqs., 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21;*

1: geneseqn1980s;*
2: geneseqn1990s;*
3: geneseqn2000s;*
4: geneseqn2001as;*
5: geneseqn2001bs;*
6: geneseqn2002as;*
7: geneseqn2002bs;*
8: geneseqn2003as;*
9: geneseqn2003bs;*
10: geneseqn2003cs;*
11: geneseqn2003ds;*
12: geneseqn2004as;*
13: geneseqn2004bs;*
14: geneseqn2005s;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	77	100.0	566 1 AAN71252	Aan71252 standard; DNA; 566 BP.
2	77	100.0	630 6 ABK14492	XX
3	77	100.0	729 1 AAN91288	XX
4	77	100.0	801 1 AAN91141	XX
5	77	100.0	840 2 AAQ66839	XX
6	77	100.0	845 2 AAQ0573	XX
7	77	100.0	845 2 AAT33293	XX
8	77	100.0	876 1 AAN80485	XX
9	77	100.0	876 1 ADP87763	XX
10	77	100.0	1092 10 ADD66285	XX
11	77	100.0	1092 12 ADI05558	XX
12	77	100.0	1092 13 ADP82120	XX
13	77	100.0	1179 10 ADP87764	XX
14	77	100.0	1179 10 ADD66286	XX
15	77	100.0	1179 12 ADP05559	XX
16	77	100.0	1179 13 ADP82121	XX
17	77	100.0	1308 1 AAN70432	XX
18	77	100.0	1308 1 AAN7765	XX
19	77	100.0	1308 10 ADD87767	XX

ALIGMENTS

20 77 100.0 1308 12 ADT05560 Adt05560 Novel rec
21 77 100.0 1308 13 ADD82122 DNA seqe Adt82122 DNA seqe
22 77 100.0 1317 2 AAO90231 HIV-1 gag Adt90231 HIV-1 gag
23 77 100.0 1320 1 AAN0351 Sequence Aan0351 Sequence
24 77 100.0 1424 1 AAN0484 Sst/BgII Adt87745 HIV-1 GAG Adt87745 HIV-1 GAG
25 77 100.0 1495 10 ADD66268 ADt66268 HIV-1 gag
26 77 100.0 1496 12 ADI05541 ADt05541 Novel rec
27 77 100.0 1496 13 ADS82103 ADs82103 DNA encod
28 77 100.0 1503 1 AAN70428 ADt87746 The DNA s Aan70428 The DNA s
29 77 100.0 1503 6 ABV78254 HIV gag D Abv78254 HIV gag D
30 77 100.0 1503 6 ABX1073 HIV gag P Abx1073 HIV gag P
31 77 100.0 1503 6 ABL91795 HIV polyn Abt91795 HIV polyn
32 77 100.0 1503 6 AAD50468 Human imm Adt50468 Human imm
33 77 100.0 1503 6 AAB8106 KING-SH C Aab8106 KING-SH C
34 77 100.0 1503 9 ADB8106 ADt73889 HIV-1 str Adm73889 HIV-1 str
35 77 100.0 1503 11 ADM736410 HIV gene Adt36410 HIV gene
36 77 100.0 1503 12 ADP65074 Adt65074 DNA seqe Adt65074 DNA seqe
37 77 100.0 1503 13 ADU81579 Adt81579 HIV-IIIB Adt81579 HIV-IIIB
38 77 100.0 1503 14 AAN92575 Sequence Aan92575 Sequence
39 77 100.0 1512 1 AAN70425 DT Adt60703 ADt60703 PI/7/24TRN
40 77 100.0 1515 10 ACC6903 Plasmid p Acc6903 Plasmid p
41 77 100.0 1515 11 ACD65074 Adt65074 DNA seqe Adt65074 DNA seqe
42 77 100.0 1515 14 AAO10574 Encodes H Aai67901 Nucleotid Aai67901 Nucleotid
43 77 100.0 1515 2 AAO10574 Encodes H Aan90350 Sequence Aan90350 Sequence

EOT

The patient claims a peptide fragment which is immunoreactive to antibodies against the HTLV-III virus and encoded for by the HTLV-III provirus nucleotide sequences selected from nucleotides 653 to 1218, 2600 to 3911, 2743 to 4211, 6619 to 7198, and 7199 to 8052. The peptide fragments are specifically recognised by antibodies produced in response

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On nucleic - nucleic search, using sw model

Run on: February 1, 2006, 10:52:42 ; Search time 405 Seconds

157.929 Million cell updates/sec

Title: US-10-604-944A-14

Perfect score: 77

Sequence: 1 ttacccatatacgacaa...aactttaatgcattggtaa 77 (without alignments)

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Searched: 6059551 seqs, 41533918 residues

Total number of hits satisfying chosen parameters: 12119102

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications NA New:*

1: /cgn2_6/prodata/2/pubpna/US08_NEW_PUB.seq:*

2: /cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq:*

3: /cgn2_6/prodata/2/pubpna/US07_NEW_PUB.seq:*

4: /cgn2_6/prodata/2/pubpna/PCT_NEW_PUB.seq:*

5: /cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq:*

6: /cgn2_6/prodata/2/pubpna/US10_NEW_PUB.seq:*

7: /cgn2_6/prodata/2/pubpna/US10_NEW_PUB.seq:*

8: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq:*

9: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq:*

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11: /cgn2_6/prodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :

Published Applications NA New:*

1: /cgn2_6/prodata/2/pubpna/US08_NEW_PUB.seq:*

2: /cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq:*

3: /cgn2_6/prodata/2/pubpna/US07_NEW_PUB.seq:*

4: /cgn2_6/prodata/2/pubpna/PCT_NEW_PUB.seq:*

5: /cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq:*

6: /cgn2_6/prodata/2/pubpna/US10_NEW_PUB.seq:*

7: /cgn2_6/prodata/2/pubpna/US10_NEW_PUB.seq:*

8: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq:*

9: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq:*

10: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq:*

11: /cgn2_6/prodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :

Published Applications NA New:*

1: /cgn2_6/prodata/2/pubpna/US08_NEW_PUB.seq:*

2: /cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq:*

3: /cgn2_6/prodata/2/pubpna/US07_NEW_PUB.seq:*

4: /cgn2_6/prodata/2/pubpna/PCT_NEW_PUB.seq:*

5: /cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq:*

6: /cgn2_6/prodata/2/pubpna/US10_NEW_PUB.seq:*

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11: /cgn2_6/prodata/2/pubpna/US60_NEW_PUB.seq:*

RESULT 1
US-10-507-928-5
; Sequence 5, Application US/10507928

; Publication No. US2005026024A1
; GENERAL INFORMATION:
; APPLICANT: POWDERMED LIMITED AND GLAXO GROUP LIMITED

; TITLE OF INVENTION: ADJUVANT
; FILE REFERENCE: N-81232B.GCW

; CURRENT APPLICATION NUMBER: US/10/507, 928

; CURRENT FILING DATE: 2004-09-17

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5

; LENGTH: 1515

; TYPE: DNA

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: nucleotide sequence of the p17/24trNEF insert in p17/24trNEF1

Query Match 100.0%; Score 77; DB 7; Length 1515;

Best local Similarity 100.0%; Pred. No. 4.3e-20;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTACCCATAGTGCAGAACATCCAGGGCAATGTGATCATCAGGCCATACCTGAAAC 60

Db 393 TTACCCATAGTGCAGAACATCCAGGGCAATGTGATCATCAGGCCATACCTGAAAC 452

; GENERAL INFORMATION:
; APPLICANT: Braun, Ralph P.

; APPLICANT: Thommen, Lindy

; APPLICANT: Van-Wely, Catherine

; APPLICANT: Ertl, Peter

; TITLE OF INVENTION: Adjuvant

; FILE REFERENCE: 033467-015

; CURRENT APPLICATION NUMBER: US/11/029, 465

EDT

C	23	24.4	31.7	1085	7	US-10-750-623-32559	Sequence 32559, A
C	24	24.2	31.4	28033	7	US-10-829-826B-42	Sequence 42, Appl
C	25	: 24.2	31.4	28033	7	US-10-829-826B-43	Sequence 43, Appl
C	26	23.8	30.9	643	8	US-11-043-752-1480	Sequence 1480, Ap
C	27	23.8	30.9	1280	7	US-10-750-185-53636	Sequence 53636, A
C	28	23.8	30.9	1280	7	US-10-750-623-53636	Sequence 13259, A
C	29	23.8	30.9	387780	7	US-10-995-561-13259	Sequence 33, Appl
C	30	23.6	30.6	480	8	US-11-219-146-33	Sequence 34, Appl
C	31	23.6	30.6	480	8	US-11-219-146-45	Sequence 45, Appl
C	32	23.6	30.6	752	8	US-11-219-146-47	Sequence 47, Appl
C	33	23.6	30.6	752	8	US-11-219-146-49	Sequence 37, Appl
C	34	23.6	30.6	752	8	US-11-219-146-49	Sequence 39, Appl
C	35	23.6	30.6	600	8	US-11-219-146-49	Sequence 41, Appl
C	36	23.6	30.6	600	8	US-11-219-146-49	Sequence 43, Appl
C	37	23.6	30.6	600	8	US-11-219-146-49	Sequence 45, Appl
C	38	23.6	30.6	752	8	US-11-219-146-49	Sequence 47, Appl
C	39	23.6	30.6	752	8	US-11-219-146-49	Sequence 37, Appl
C	40	23.6	30.6	752	8	US-11-219-146-49	Sequence 19, Appl
C	41	23.6	30.6	752	8	US-11-219-146-49	Sequence 23, Appl
C	42	23.6	30.6	1151	8	US-11-219-146-49	Sequence 1, Appl
C	43	23.6	30.6	1151	8	US-11-219-146-49	Sequence 3, Appl
C	44	23.6	30.6	1151	8	US-11-219-146-49	Sequence 5, Appl
C	45	23.6	30.6	1151	8	US-11-219-146-49	Sequence 7, Appl

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GenCore version 5.1.7
101331 Sequence 1
105038 Sequence 6
AB112051 Human imm
AB112052 Human imm
AB112056 Human imm
AB112059 Human imm
AY660925 HIV-1 iso
A06256 PXX460 gag
AF071303 HIV-1 iso
AF070634 HIV-1 iso
179824 Sequence 1
AR044674 Sequence
I38635 Sequence 3
I40606 Sequence 3
A02736 Artificial
AY56080 HIV-1 iso
AY134961 HIV-1 iso
AY134965 HIV-1 iso
AY134966 HIV-1 iso
AY134957 HIV-1 iso
AY134959 HIV-1 iso
AY134967 HIV-1 iso
B01254 DNA encoding
A02442 Artificial
A19610 Artificial
A75992 Sequence 3
A75896 Sequence 7

Om nucleic - nucleic search, using sw model
Run on: February 1, 2006, 10:39:26 ; Search time 2175 Seconds
(without alignments)
2012.389 Million cell updates/sec

Title: US-10-604-944a-14
Perfect score: 77

Sequence: 1 ttacccatatagtgcagaaca.....aactttaatgcatggtaa 77

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing First 45 summaries

Database : GenEmbl:*

- 1: gb_ba:*
- 2: gb_in:*
- 3: gb_env:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pr:*
- 9: gb_ro:*
- 10: gb_st:*
- 11: gb_BY:*
- 12: gb_un:*
- 13: gb_vl:*
- 14: gb_htg:*
- 15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match length DB ID

Description

Result No.	Score	Query	Match length	DB	ID	Description
1	77	100.0	303	13	HIVM3S1	HIVM3S1
2	77	100.0	303	13	HIVM4S1	Human immunodeficiency virus type 1, myristylated gag protein p17 (gag) gene, partial cds.
3	77	100.0	303	13	HIVM5S1	Human immunodeficiency virus type 1, myristylated gag protein p17 (gag) gene, partial cds.
4	77	100.0	303	13	HIVM6S1	Human immunodeficiency virus type 1, myristylated gag protein p17 (gag) gene, partial cds.
5	77	100.0	303	13	HIVN9S1	Human immunodeficiency virus type 1, myristylated gag protein p17 (gag) gene, partial cds.
6	77	100.0	330	13	AB154280	Human immunodeficiency virus type 1, myristylated gag protein p17 (gag) gene, partial cds.
7	77	100.0	330	13	AB154285	Human immunodeficiency virus type 1, myristylated gag protein p17 (gag) gene, partial cds.
8	77	100.0	330	13	AB154295	Human immunodeficiency virus type 1, myristylated gag protein p17 (gag) gene, partial cds.
9	77	100.0	425	13	AY103237	Human immunodeficiency virus type 1, myristylated gag protein p17 (gag) gene, partial cds.
10	77	100.0	426	13	AY103239	Human immunodeficiency virus type 1, myristylated gag protein p17 (gag) gene, partial cds.
11	77	100.0	426	13	AY103240	Human immunodeficiency virus type 1, myristylated gag protein p17 (gag) gene, partial cds.
12	77	100.0	426	13	AY103241	Human immunodeficiency virus type 1, myristylated gag protein p17 (gag) gene, partial cds.
13	77	100.0	426	13	AY103242	Human immunodeficiency virus type 1, myristylated gag protein p17 (gag) gene, partial cds.
14	77	100.0	426	13	AY103243	Human immunodeficiency virus type 1, myristylated gag protein p17 (gag) gene, partial cds.
15	77	100.0	451	13	AF017925	Human immunodeficiency virus type 1, myristylated gag protein p17 (gag) gene, partial cds.
16	77	100.0	502	13	AF116068	Human immunodeficiency virus type 1, myristylated gag protein p17 (gag) gene, partial cds.
17	77	100.0	517	13	AF116050	Human immunodeficiency virus type 1, myristylated gag protein p17 (gag) gene, partial cds.
18	77	100.0	536	13	AB112053	Human immunodeficiency virus type 1, myristylated gag protein p17 (gag) gene, partial cds.

ALIGNMENTS

E D T

RESULT 1

HIVM3S1

Human immunodeficiency virus type 1, myristylated gag protein p17 (gag) gene, partial cds.

DEFINITION 303 bp ss-RNA linear VRL 23-NOV-1993

ACCESSION 121498

VERSION 121498.1 GI:424696

KEYWORDS gag gene; myristylated gag protein p17.

SOURCE Human immunodeficiency virus 1 (HIV-1).

ORGANISM Human immunodeficiency virus 1.

VIRUSES; Retro-transcribing viruses; Retroviridae;

Orthoretrovirinae; Lentivirus; Primate lentivirus group.

REFERENCE 1 (bases 1 to 303)

AUTHORS Zhu,T., Mo,H., Wang,N., Nam,D.S., Cao,Y., Koup,R.A. and Ho,D.D.

JOURNAL Genotypic and phenotypic characterization of HIV-1 patients with primary infection

SCIENCE 261 (5125), 1179-1181 (1993)

PUBMED 8356453

COMMENT Original source text: Human immunodeficiency virus type 1 RNA.

FEATURES Location/text: Human immunodeficiency virus type 1 RNA.

source 1..303

/organism="Human immunodeficiency virus 1"
/mol_type="genomic RNA"
/db_xref=taxon:11676"

gene 1..303

/gene="gag"
<1..>303

/gene=gag"

/codon_start=1
/db_xref=taxon:11676"

/product="myristylated gag protein p17"

/protein_id="AAH44822.1"

/db_xref=UniProtKB:Q42697

/translation="KQPAIOLGSEERLSLENTVATLYCHOKIDVYDTEEALKRKEE

QNSKKEKAQDAGTENSSQSVONPIVONIQGMVHQALSPRTLNWKVVEEKAP"

ORIGIN

Query Match 100.0%; Score 77; DB 13; length 303;

Best Local Similarity 100.0%; Pred. No. 8.2e-16; Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTACCTATAGTCAGACATCCAGGGCAAATGGTACATCAGGCCATACCTAGAAC 60